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Multi-agents Modeling and Simulation of the Spread of Tuberculosis in the City of Ngaoundéré (Cameroon)

Gazissou Balama[a]*, Kamla Vivient Corneille[b]

[a]*Department of Mathematics and Computer Science, Faculty of Sciences, University of Ngaoundéré, Cameroon*

[b]*Department of Mathematics and Computer Science, ENSAI, University of Ngaoundéré, Cameroon*

[a]*Email: gazissoubalraph@gmail.com*

[b]*Email: vckamla@gmail.com*

Abstract

In this paper, a model based on Multi-Agent Systems (MAS) of the spread of tuberculosis in the city of Ngaoundéré is proposed. After studying the behavior of the population and treatment using the software "OpenJUMP" of the satellite image of the city of Ngaoundéré, a multi-agent modeling of the population including individual activities, contraction and evolution of tuberculosis is made. This modeling followed the Gaia approach and used the modeling language AUML. The satellite image was processed in the integrated simulation platform GAMA and simulations were made. The simulation results show that in the absence of treatment, the rate of spread of tuberculosis in the city of Ngaoundéré, denoted T_0 strongly depends on the behavior of individuals, the quantity of Koch Bacillus (BK) released by a sick individual, the life of a BK in the air. The analysis of T_0 shows that there is a threshold beyond which the disease is endemic and below which it disappears.

Keywords: AUML; Gaia; GAMA; Koch Bacillus; Multi-Agent System; OpenJUMP; tuberculosis; velocity.

1. Introduction

Tuberculosis is an endo-epidemic disease caused by Koch's Bacillus (BK), also known as Mycobacterium Tuberculosis (MT), which is mainly transmitted by air [1]. There is a form of tuberculosis that is transmitted from cattle to humans. It is caused by Bovis Mycobacterium, which is widely present in cattle breeding areas. Bovis Mycobacterium is transmitted in partially cooked meat and unboiled fresh milk [2]. There is pulmonary tuberculosis and bone tuberculosis. Pulmonary tuberculosis accounts for 80% of tuberculosis cases.

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* Corresponding author.

There are three types of pulmonary tuberculosis, we can cite pulmonary tuberculosis with positive expectoration under microscopic examination (M+), pulmonary tuberculosis with positive expectoration only in culture (C+) and pulmonary tuberculosis with negative expectoration in culture (C_0). Pulmonary tuberculosis in adults is generally smear-positive and therefore highly contagious. People with pulmonary tuberculosis are spreading the disease. Approximately 20 people per year are estimated to be infected by positive microscopic pulmonary tuberculosis (MPT+) patient [2].

According to WHO estimates in 2006, 1/3 of the world's population was infected, 9.2 million new cases, of which approximately 50% were M + patients, an increase of 0.6% compared to 2005 and the disease index was 139/100 000 and there were 1.7 million deaths [3]. Faced with this scourge, the researchers did not remain indifferent. In medicine and biology several researches have been carried out and they continue to be made.

We can cite for example the works of Nadia Ait-Khaled and Donald Enarson in 1999 [2], those of Boulahbal and Chaulet in 2004 [4], those of Lemaître in 2009 [5] and the work of Pierre Aubry in 2011[1].

Mathematicians have also focused on this axis of research and have devised deterministic models. For example, in 1999 Castillo-Chavez and his team proposed a simple model on tuberculosis without exogenous reinfection. In the same year, Zhilan Feng and his team proposed a model with exogenous reinfection [6]. In 2002, Baojun Song and his team proposed a model with dynamic slow and fast transmission [7]. In 2010, Samuel Bowong and his team proposed a model with N latent classes [8]. In 2011, Jean Jules Tewa and his team proposed a two-patch model on tuberculosis with migration in all compartments [9] and a year later they proposed a two-patch model with several levels of progression and migration between susceptibles [10].

All these deterministic models are models in homogeneous compartments that reflect the dynamics of transmission of tuberculosis by differential equations. However, in these deterministic models, there is a lack of connection with certain forms of real data, which often gives them a speculative form. Moreover, they are aggregated models (they are not flexible) and they are not individual-centered.

The resulting problem is thus: Can we design an individual-centered model capable of showing the dynamics of the spread of tuberculosis and which is flexible (able to provide additional information when it is transplanted with other modules, without modifying its internal structure)?

In several computer studies, it has been found that there is a new branch of artificial intelligence, which offers the possibility of directly representing individuals with their behaviors and their interactions, which easily integrates the spatial dynamics (displacements linked to the activities) and who can build flexible models: these are the Multi-Agent Systems (MAS). In 2011, for example, Gabriel Guilsou Kolaye was able to model the spread of a cholera epidemic using MAS [11]. In 2013, Tchawa Ganga modeled the communication between hives of bees in a closed system [12].

The aim of this work is to use Multi-Agent Systems to design a model of the dynamics of the spread of tuberculosis.

Our study is limited to tuberculosis transmissible from man to man, and to patients with TPM +. And we assume that all newborns and immigrants are susceptible and we will not consider cases of treatment.

2. Materials and methods

2.1. The MAS

MAS is a set of agents interacting, most often, according to modes of cooperation, competition or coexistence. According to Feber [13], it is a system composed of an environment E, a set of objects O, a set of agents A, a set of relations R and a set of operators Op. A Russell agent is an entity that perceives and acts on its environment [14].

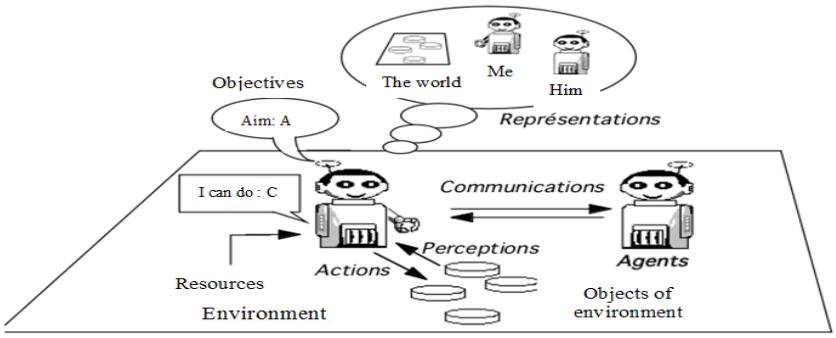

Figure 1: An agent in interaction with its environment and with other agents

2.2. Presentation of Gaia's methodology version 2

The following figure shows the steps of the Gaia's methodology[15] version 2 that we have followed during our modeling.

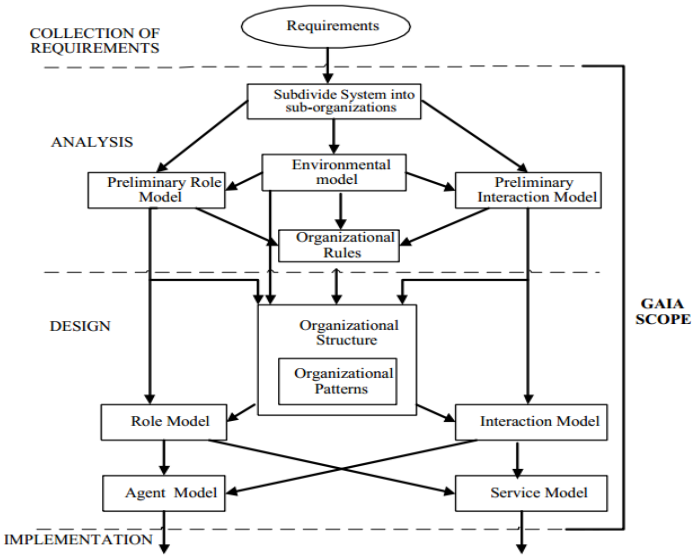

Figure 2: Detailed diagrams of the steps of the Gaia V2 methodology

3. Results and Discussions

3.1. Presentation of the model

3.1.1. Description of the system and subdivision into subsystems

The dynamics of the spread of tuberculosis is linked to the dynamics of the population, because the spread of tuberculosis derives from the displacement of sick people's milieu. Individuals have daily activities that make them adopt different behaviors. Among these individuals are those who attend schools, others work in the public or private services of the city. Most people also regularly attend the markets. Among the individuals, there are those who belong to the Muslim religion, those who belong to the Christian religion and those who do not belong to any religion. People who belong to the Muslim religion go to the mosque at least five times a day for prayers that last at least 5 minutes. Those who belong to the Christian religion frequent the churches much more on weekends for cults that last for 1h30min. An individual may have several daily activities, but these activities are organized so that two activities cannot be performed at the same time. For example, an individual can go to work in the morning, in the afternoon he goes to the market, towards the end of the afternoon he can go to leisure centers for entertainment, Evening he goes home to rest and spend all night and the morning after his activities begin again. The activities of an individual can vary according to the days. For example, an individual's activities on weekends are different from his or her activities during other days of the week. In the city of Ngaoundéré in Cameroon, houses, shops in markets, places of service, hospitals and sometimes even classrooms are a bit ventilated places where people group together most often: areas conducive to the spread of tuberculosis. To facilitate our modeling we have subdivided our system into seven subsystems: houses, schools, markets, service locations, hospitals, mosques and churches.

3.1.2. Environmental model

Here it is a question to bring out on the satellite image of the city of Ngaoundéré the different subsystems in order to obtain our model of environment. To achieve this we have processed our image using the OpenJUMP software[16].

Figure 3: Satellite image of our study area

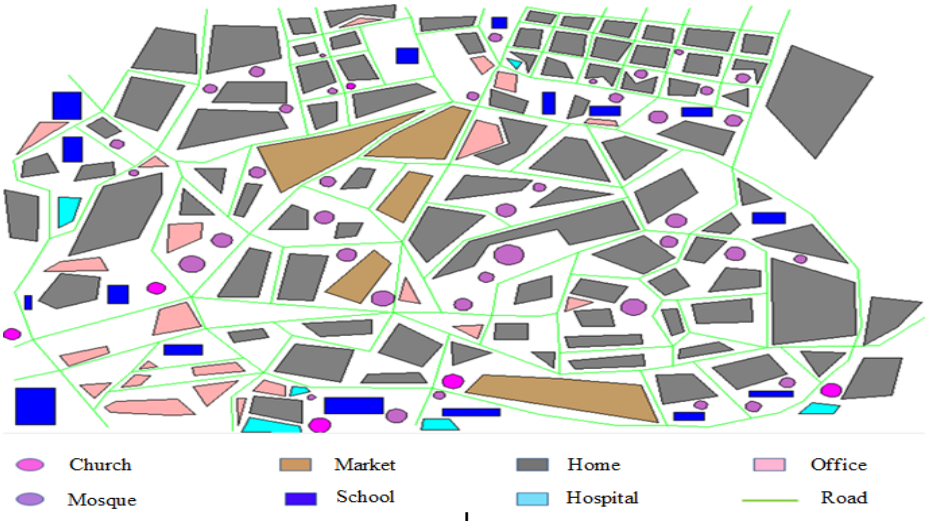

Figure 4: Environmental model obtained (image processed)

3.1.3. Role Model and Organizational Structure

The organizational diagram in Fig.5 presents our general system with the different roles that can be found in the different subsystems.

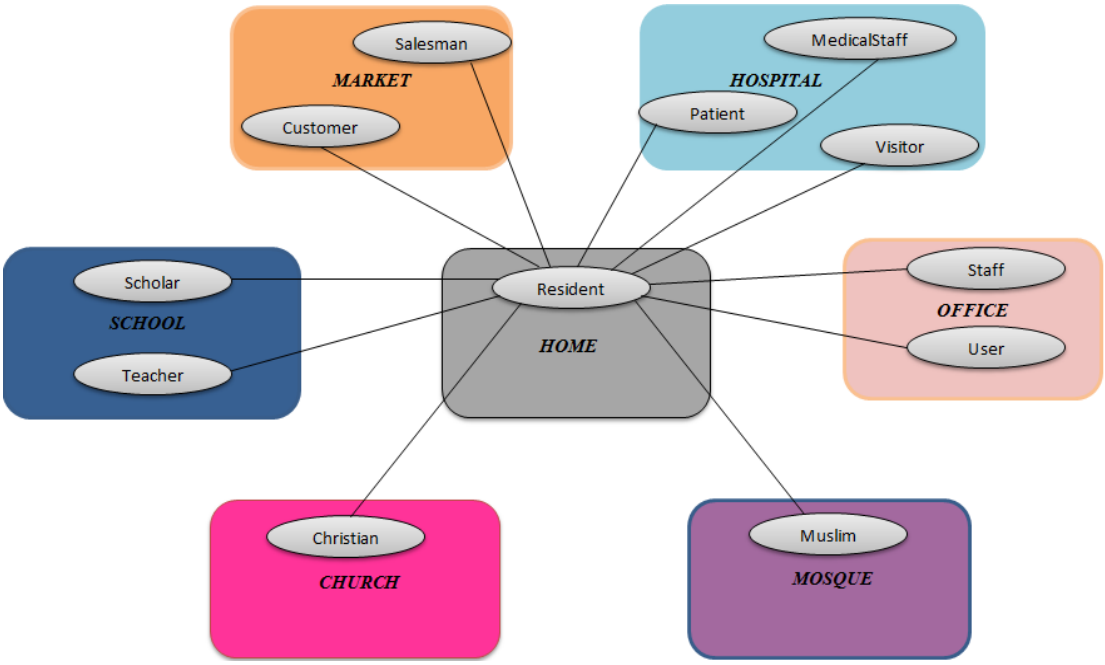

Figure 5: Organizational diagram

We present in Table 1 the permissions and responsibilities of each role according to the role model. Let us first define the variables important for our modeling.

The sphere of infection of an individual: represents the area in which the individual can infect another individual if he is sick. *The radius of infection denoted* ***R_inf***: is the distance that represents the radius of the sphere of infection.

Density_BK: it is a variable which determines at a given instant t, the quantity of BK contained in the air which is in the sphere of infection of any individual.

Table 1: Role Model

Roles	**Permissions**	**Responsibilities**
SCHOLAR	**Read**: desk; distance_desk; **Modify**: density_BK; deskt; distance_ desk;	**vivacity**: breathe^{w}||([speak^{+}]|[move^{+}]|cough*) **surety**: 0 <= density_BK <= $\frac{2\pi(R\_inf)^3}{3}$
TEACHER	**Read**: seat; **Modify**: density_BK ; seat;	**vivacity**: breathe^{w}|| speak $^{+}$||move^{+}|| cough * **surety** : 0 <= density_BK <= $\frac{2\pi(R\_inf)^3}{3}$
SALESMAN	**Modify**: density_BK;	**vivacity**: breathe^{w}|| speak $^{+}$||move^{+}|| cough * **surety** : 0 <= density_BK <= $\frac{2\pi(R\_inf)^3}{3}$
STAFF USER	**Read**: seat; distance_ seat; **Modify**: density_BK ; seat;distance_ seat;	**vivacity**: breathe^{w}|| speak $^{+}$||move*|| cough * **surety**: 0 <= density_BK <= $\frac{2\pi(R\_inf)^3}{3}$
CUSTOMER	**Read**: seat; distance_ seat; **Modify**: density_BK ; seat; distance_ seat;	**vivacity**: breathe^{w}|| speak $^{+}$||move^{+}|| cough * **surety**: 0 <= density_BK <= $\frac{2\pi(R\_inf)^3}{3}$
CHRISTIAN	**Read**: seat; distance_ seat; **Modify**: density_BK ; seat; distance_ seat;	**vivacity**: breathe^{w}|| speak *||[move^{+}]|| cough * **surety**: 0 <= density_BK <= $\frac{2\pi(R\_inf)^3}{3}$
MUSLIM	**Modify**: density_BK	**vivacity**: breathe^{w}|| speak *||move*|| cough * **surety**: 0 <= density_BK <= $\frac{2\pi(R\_inf)^3}{3}$
MEDICAL_STAFF, PATIENT, VISITOR, RESIDENT	**Read**: seat; bed ; **Modify**: density_BK; seat; bed ;	**vivacity**: breathe^{w}|| speak $^{+}$||move^{+}|| cough * **surety**: 0 <= density_BK <= $\frac{2\pi(R\_inf)^3}{3}$

x.y means **x** followed by **y** ;

x|y means that **x** or **y** occurs ;

$\mathbf{x}^{*}$ means that **x** appears 0 or more times ;

$\mathbf{x}^{+}$ means that **x** occurs one or more times ;

$\mathbf{x}^{w}$ means that **x** often occurs indefinitely ;

[x] means that **x** is optional ;

x||y means that no matter the order of appearance of **x** and **y**.

3.1.4. Interaction Model

Let X be an individual who has a sick state and plays the role of a resident at home, a student at school and a client at the market. The X entity can infect other inhabitants with whom it lives at home; At school he can infect his nearest classmates and also his teacher; At the market, it can infect other customers and also the traders. This scenario is realized by the sequence diagram of Fig. 6.

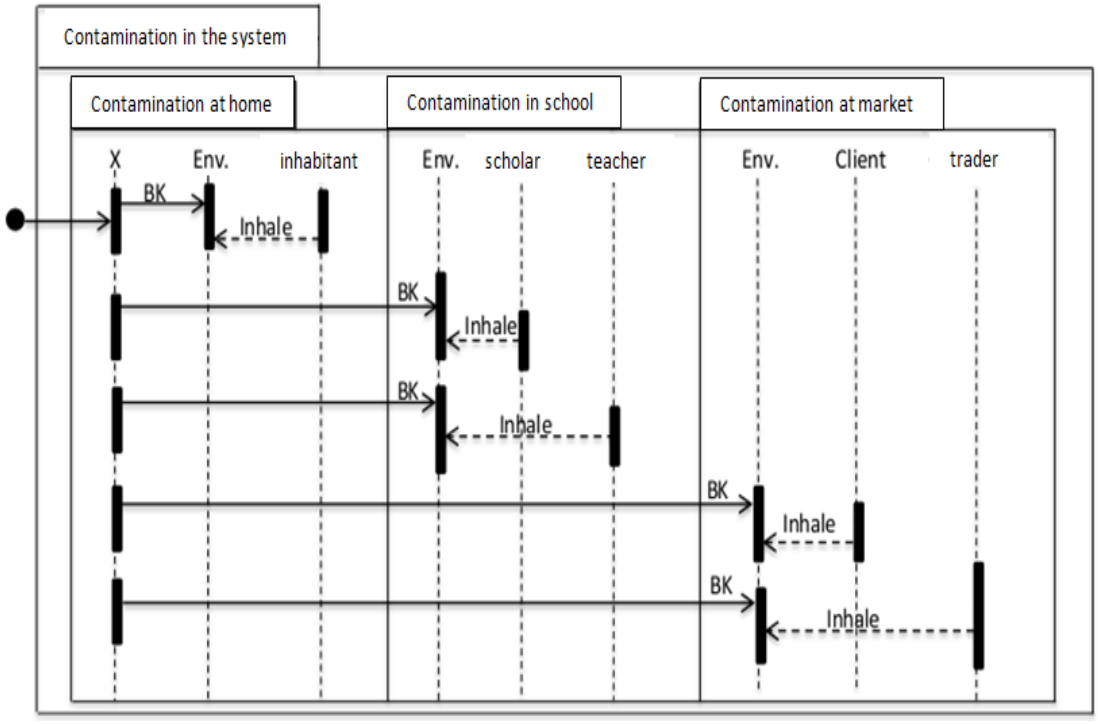

Figure 6: Sequence diagram of a contamination in the system

Different states that an agent of our system can have are shown in the transition state diagram of Fig.7.

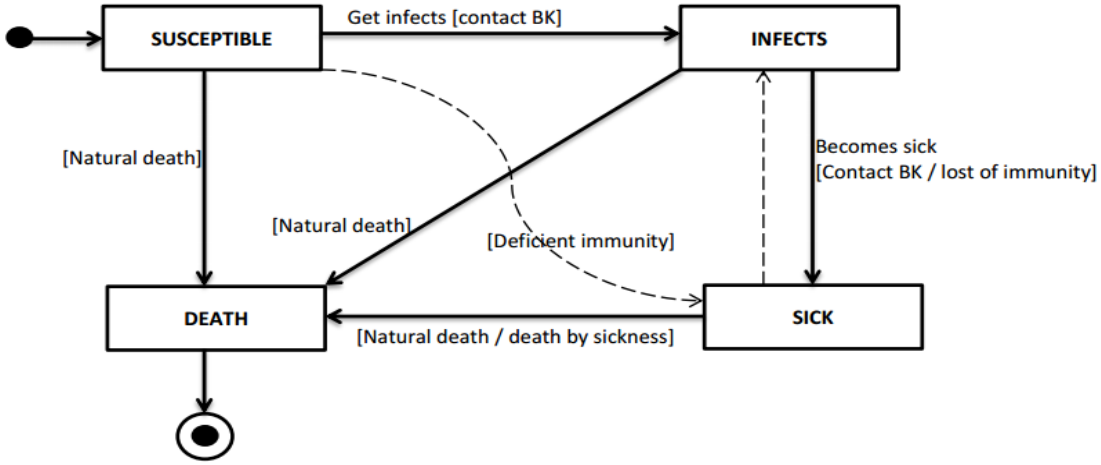

Figure 7: Transition state diagram of infection status

3.1.5. Organizational rules

To ensure the proper functioning of the system, the following five safety rules must be respected: 1) ¬ *(Teacher | Scholar)*: means that an entity (agent) playing the role of a pupil cannot play the role of a Teacher, vice versa;

2) ¬ *(User | Staff)*;

3) ¬ *(Christian | Muslim);*

4) ¬ *(Teacher | Medical Staff | Staff);*

5) ¬ *(Scholar | Staff | Medical_Staff).*

3.1.6. Agent models

Resident ^{1} *play* $\rightarrow$ *Teacher, Customer, User, (Christian|Muslim), (Visitor|Patient)* : This expression means that one instance of the class of Resident agent may play the roles Teacher, Customer, User, Christian or Muslim and Visitor or Patient.

Resident ^{1} *play* $\rightarrow$ *Scholar, Customer, User, (Christian|Muslim), (Visitor|Patient)*

Resident ^{1} *play* $\rightarrow$ *Staff, Customer, User, (Christian|Muslim), (Visitor|Patient)*

Resident ^{1} *play* $\rightarrow$ *Medical_staff, Customer, User, (Christian | Muslim), (Visitor |Patient)*

Resident ^{1} *play* $\rightarrow$ *Salesman, Customer, User, Scholar, (Christian | Muslim), (Visitor |Patient).*

3.1.7. Service Model

For the infection in the system (passage from a healthy to infected state), the service model is represented as follows:

Entry: living Koch bacilli are released into the air (variable densite_BK is full);

Output: the healthy agent inhales the bacilli contained in the variable *densite_BK*;

Precondition: the presence of a contagious sick agent is necessary and a healthy agent with good immunity must be present for at least 1 hour near the diseased agent.

Post condition: the agent who inhaled the BK became infected.

For the contamination in the system (passage from an infected to sick state), the service model is represented as follows:
Entry: living Koch bacilli are released into the air (the variable densite_BK is full);

Output: the healthy or infected agent inhales the bacilli contained in the variable densite_BK;

Precondition: An infectious agent must be present and a healthy agent with good immunity must be present for at least 6 hours near the diseased agent or that an agent already infected and with good immunity passes less than 6 hours near the patient.

Post condition: The agent inhaling the BK exhibits the symptoms of a sick individual.

Table 2: Script in GAML showing infection and contamination

Script in GAML showing an infection	**Script in GAML showing contamination**

reflex become_infecte when: (est_susceptible or (est_malade and flip(gn)))
{
set V_s_inf <- (R_inf)^3*2.093;
set P_inf <- densite_BK / V_s_inf ;
if (flip(beta * P_inf)) {
set est_susceptible <- false;
set est_infecte <- true;
set est_malade <- false;
set color <- rgb('yellow');
set location <- any_location_in(living_place);
}
}
	reflex become_malade when: ((est_infecte) or (est_susceptible and imunite))
	{
	if(flip(delta * P_inf))
	{
	set est_susceptible value: false;
	set est_infecte value: false;
	set est_malade value: true;
	set color value: rgb('red');
	set location <- any_location_in(living_place);
	}
	}

3.2. Simulation environment and calculation of the basic reproduction rate

The simulation parameters are presented in Table 3.

Table 3: Simulation Parameters

Data	**Sources**
nombre_S = 2500 (Number of healthy)	Sample
nombre_E = 100 (Number of infected)	Sample
nombre_I = 100 (Number of sick)	Sample
d = 1/(2*365*24*60) (lethality rate)	Regional Hospital of Ngaoundéré
nu = 1/(49*365*24*60) (mortality rate)	National Institut of statistical
gn = 1/(2*365*24*60) (natural healing rate)	(N. Lemaître, 2009), Regional Hospital of Ngaoundéré
beta = 0.005 (contact rate Susceptible->Infect)	Sample
delta = 0.001 (contact rate Infect->Sick)	Sample
density_BK = 100 (Density des bacilli)	Sample
R_inf = 3 (radius of infection)	Sample

The figure 8 represent the simulation environnement.

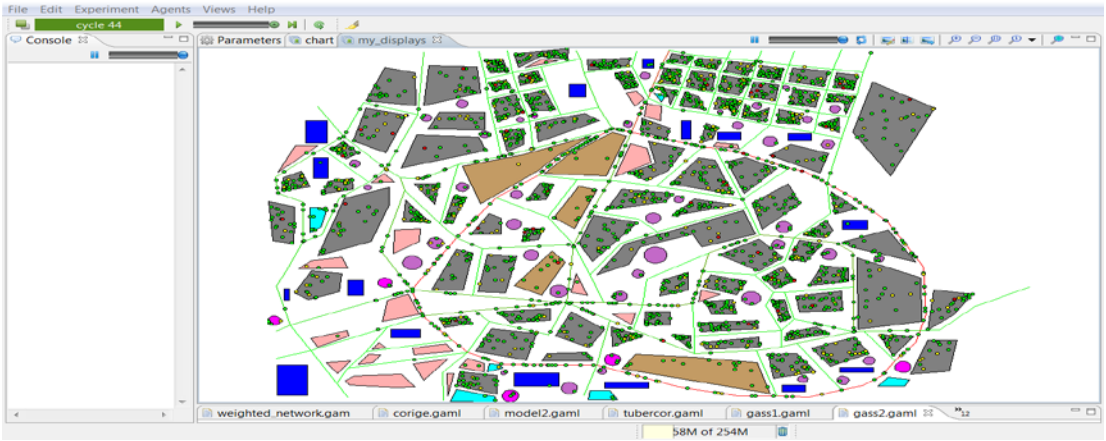

Figure 8: Simulation Environment

In this figure the green dots represent the healthy agents, the yellows are the infected and the reds the sick. Our basic reproduction rate, which we note T_0, is calculated as follows: we introduce a diseased agent into our environment among a population of susceptible agents and we write a batch code in which we run 15 simulations. The outputs of each simulation are stored in files. Later, in each of the 15 files, we will see the number of individuals who have been infected by our sick agent throughout their lives. Then, an arithmetic mean of the numbers of infected individuals is calculated to find the average number of secondary cases generated by our sick individual.

3.3. Results of simulations

In this part, we simulate our model to explore the role that the threshold parameter T_0 can play in the evolution of the different epidemiological classes. First, we assume that $\beta = 3.01$ and $\delta = 0.01$. In this case, $T_0 = 273.636$ and the result of the simulations is given in FIG. 9. It is noted that the number of patients is greater than the number of susceptible. This is due to the fact that T_0 is very large.

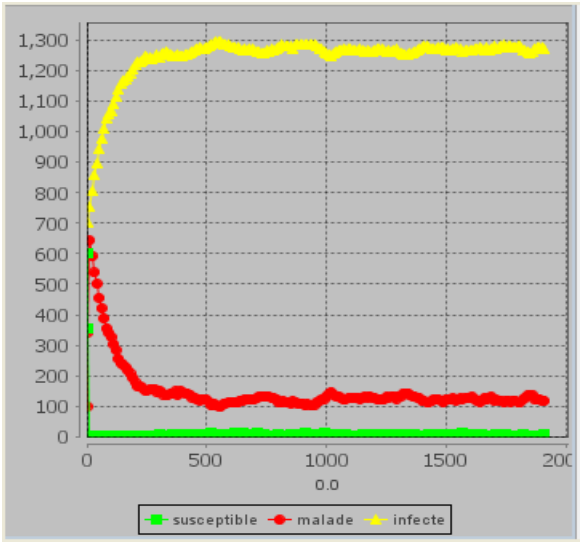

Figure 9: Result for $T_0 = 273.636$

In a second step, we assume that $\beta = 0.35$ and $\delta = 0.01$. In this case, $T_0 = 31.818$ and the result of the simulations is given in FIG. 10. We note that the number of patients is always greater than the number of susceptible. But unlike Figure 9, the probability curve is above 3. This is due to the fact that T_0 is always large.

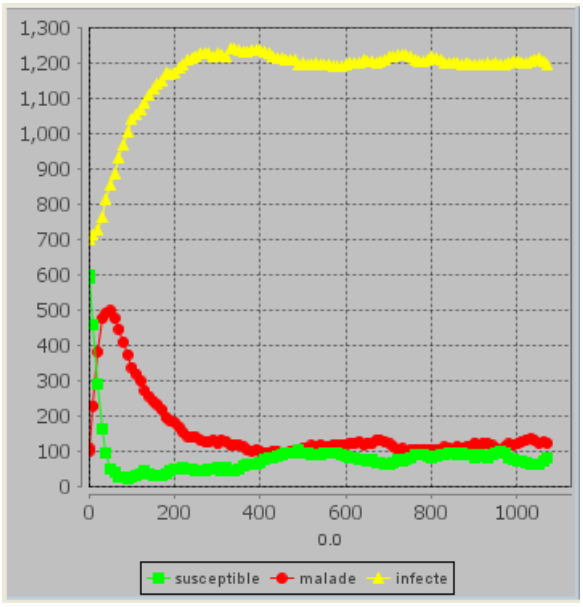

Figure 10: Result for $T_0 = 31.818$

We assume that $\beta = 0.449$ and $\delta = 0.21$. In this case, $T_0 = 2.132$ and the result of the simulations is given in Fig. 11.

It is observed that the patients disappear after 50 days and the curve of the susceptible grows and passes over that of the infected after 400 days. This is due to the fact that T_0 has become smaller.

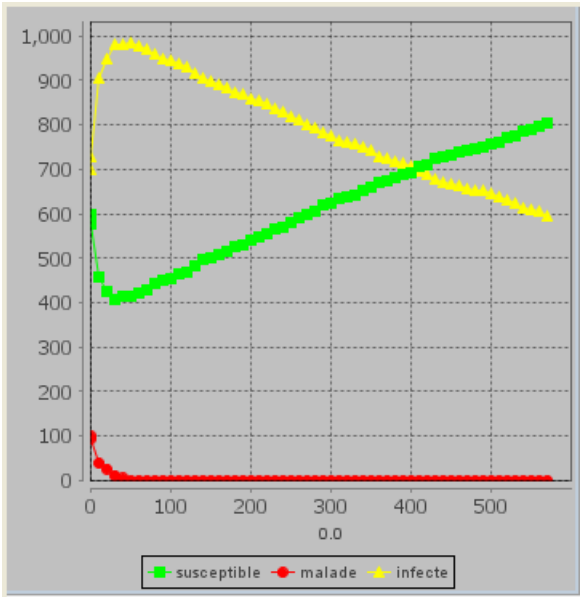

Figure 11: Result for $T_0 = 2.132$

If we assume that $\beta = 0.05$ and $\delta = 0.21$, then $T_0 = 0.236$ and the result of the simulations is given in Fig.12. It is observed that the patients disappear, the number of infected decreases more rapidly and tends more and more towards 0 and the number of susceptible grows and passes over that of the infected after 150 days. This is due to the fact that $T_0 < 1$.

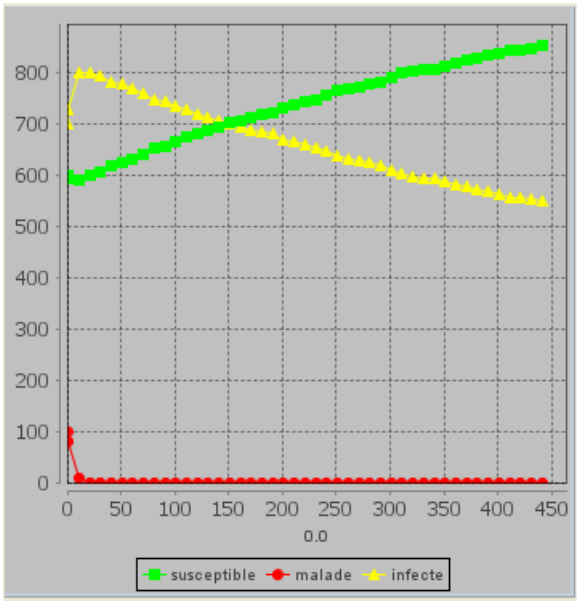

Figure 12: Result for $T_0 = 0.236$

3.4. Sensitivity analysis

The sensitivity analysis method that we use is the local sensitivity analysis, which consists in: varying the input parameters one by one on a few points (± 10%, ± 50%); Performing the simulations for each of the points (30 simulations); Calculating the means of the outputs obtained by parameter set; Calculate the sensitivity indices and the percentages of variations [17].

The curves in Fig. 13 show the sensitivity analyzes of the contact rate parameter. On these curves, it can be seen that the greater the rate of contact, the greater the number of patients and infected.

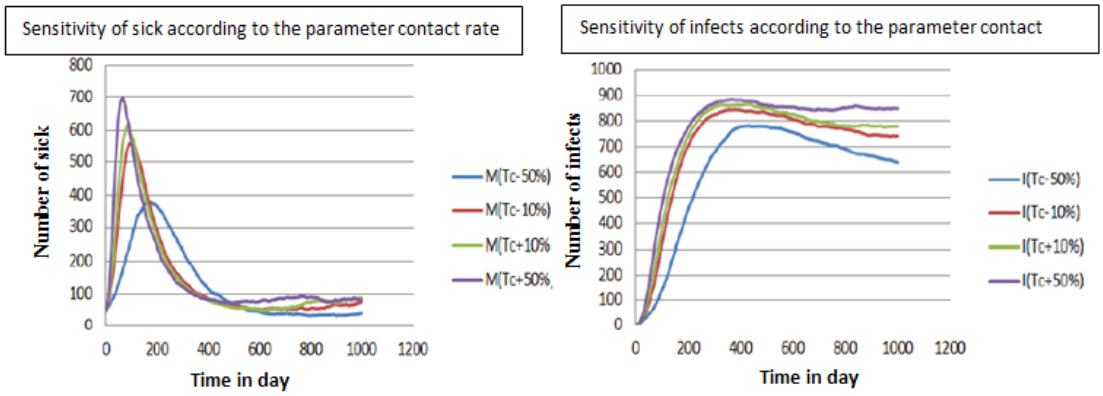

Figure 13: Contact Rate and Illness

The curves in Fig.14 show the sensitivity analyzes of the patient-healthy distance parameter. One notices on these curves that the greater this parameter, the less chance of getting infected and becoming ill.

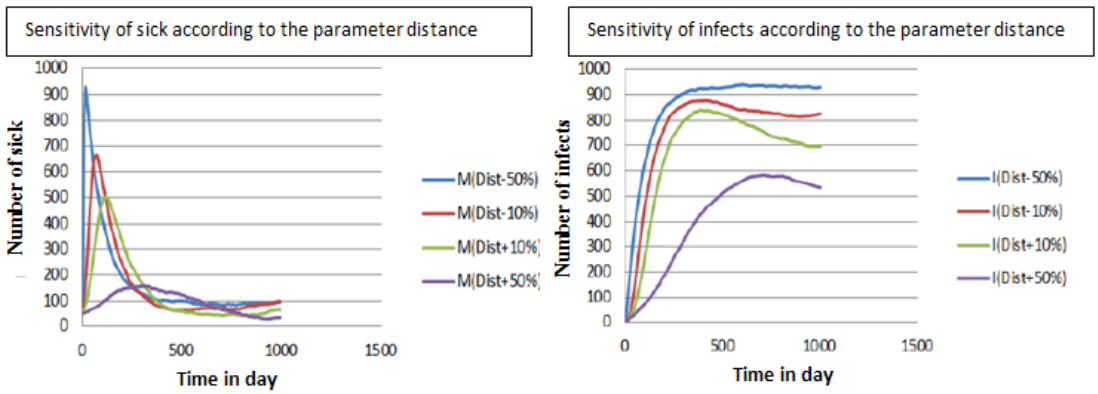

Figure 14: Distance and disease

The curves in Fig.15 show the sensitivity analyzes of the density_BK parameter.

It is found on these curves that the larger the parameter, the more the number of patients and infected increases.

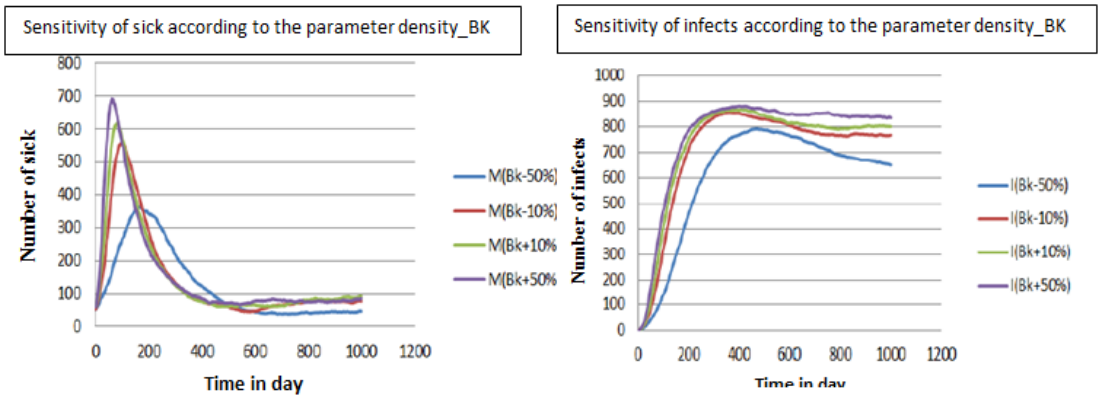

Figure 15: Density_BK and disease

Legends of the curves are defined as follows:

- M (Tc +/- x%): defines the curve of patients according to the basic input parameter "contact rate" modified to +/- x%.

- I (Tc +/- x%): defines the infected curve according to the basic input parameter "contact rate" modified to +/- x%.

- M (Dist +/- X%): define the patient curve according to the basic input parameter "distance" modified to +/- x%.

- I (Dist +/- x%): define the infected curve according to the basic input parameter "distance" modified to +/- x%.

- M (Bk +/- x%): defines the curve of the patients according to the basic input parameter "density_BK" modified to +/- x%.

- I (Bk +/- x%): defines the curve of the infected according to the basic input parameter "density_BK" modified to +/- x%.

4. Conclusion

In this paper we proposed a model of the spread of tuberculosis based on MAS. This model was designed following the steps of the Gaia V2 methodology. We have implemented and simulated our model in the GAMA platform [17]. Sensitivity analyzes showed that the baseline reproduction rate T_0 decreases with the rate of contact between the susceptible and the sick and that the spread of tuberculosis depends on the density of the bacilli in the air and the distance between the sick and the susceptible. In perspective we consider to improve the model by taking into account the treatments, because in our model we first focused on three compartments (the susceptible, the infected and the sick). We also plan to do a multi-patch model of MAS-based tuberculosis and deploy it in distributed simulation environments to optimize simulation time.

5. Recommendations

As recommendations, we propose that the Cameroonian government organize TB screening campaigns to detect disease cases and therefore take steps to isolate patients at MPT+ for treatment. Because, according to our sensitivity analyzes, the baseline reproduction rate T_0 decreases with the rate of contact between the susceptible and the sick and that the spread of tuberculosis depends on the density of the bacilli in the air and the distance between the sick and the susceptible.

We also propose to the government to make the population aware of the risks of contamination and the hygiene of life to adopt to eradicate this scourge.

Acknowledgements

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